RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/643,801A_

Source: _16000 – EF'S_

Date Processed by STIC: _6-28-05_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 06/28/2005
PATENT APPLICATION: US/10/643,801A   TIME: 15:14:22

Input Set : N:\efs\10643801A_efs\RTS0678USSEQ.txt
Output Set: N:\CRF4\06282005\J643801A.raw

```
   3 <110> APPLICANT: Sanjay Bhanot
   4         Kenneth W. Dobie
   6 <120> TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
   8 <130> FILE REFERENCE: RTS-0678US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/643,801A
C--> 10 <141> CURRENT FILING DATE: 2003-08-18
  10 <160> NUMBER OF SEQ ID NOS: 233
  13 <210> SEQ ID NO: 1
  14 <211> LENGTH: 20
  15 <212> TYPE: DNA
  16 <213> ORGANISM: Artificial Sequence
  18 <220> FEATURE:
  20 <223> OTHER INFORMATION: Antisense Oligonucleotide
  22 <400> SEQUENCE: 1
  23 tccgtcatcg ctcctcaggg                                        20
  26 <210> SEQ ID NO: 2
  27 <211> LENGTH: 20
  28 <212> TYPE: DNA
  29 <213> ORGANISM: Artificial Sequence
  31 <220> FEATURE:
  33 <223> OTHER INFORMATION: Antisense Oligonucleotide
  35 <400> SEQUENCE: 2
  36 gtgcgcgcga gcccgaaatc                                        20
  39 <210> SEQ ID NO: 3
  40 <211> LENGTH: 20
  41 <212> TYPE: DNA
  42 <213> ORGANISM: Artificial Sequence
  44 <220> FEATURE:
  46 <223> OTHER INFORMATION: Antisense Oligonucleotide
  48 <400> SEQUENCE: 3
  49 atgcattctg cccccaagga                                        20
  52 <210> SEQ ID NO: 4
  53 <211> LENGTH: 2439
  54 <212> TYPE: DNA
  55 <213> ORGANISM: H. sapiens
  57 <220> FEATURE:
  59 <220> FEATURE:
  60 <221> NAME/KEY: CDS
  61 <222> LOCATION: (231)...(1397)
  63 <400> SEQUENCE: 4
  64 ctccgggaac gccagcgccg cggctgccgc ctctgctggg gtctaggctg tttctctcgc   60
  66 gccaccactg gccgccggcc gcagctccag gtgtcctagc cgcccagcct cgacgccgtc  120
  68 ccgggacccc tgtgctctgc gcgaagccct ggccccgggg gccggggcat gggccagggg  180
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```
70  cgcggggtga agcggcttcc cgcggggccg tgactgggcg ggcttcagcc  atg aag  236
71                                                          Met Lys
72                                                           1
74  acc ctc ata gcc gcc tac tcc ggg gtc ctg cgc ggc gag cgt cag gcc  284
75  Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu Arg Gln Ala
76           5               10                  15
78  gag gct gac cgg agc cag cgc tct cac gga gga cct gcg ctg tcg cgc  332
79  Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro Ala Leu Ser Arg
80       20                  25                  30
82  gag ggg tct ggg aga tgg ggc act gga tcc agc atc ctc tcc gcc ctc  380
83  Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser Ala Leu
84  35                  40                  45              50
86  cag gac ctc ttc tct gtc acc tgg ctc aat agg tcc aag gtg gaa aag  428
87  Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val Glu Lys
88               55                  60                  65
90  cag cta cag gtc atc tca gtg ctc cag tgg gtc ctg tcc ttc ctt gta  476
91  Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe Leu Val
92               70                  75                  80
94  ctg gga gtg gcc tgc agt gcc atc ctc atg tac ata ttc tgc act gat  524
95  Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys Thr Asp
96           85                  90                  95
98  tgc tgg ctc atc gct gtg ctc tac ttc act tgg ctg gtg ttt gac tgg  572
99  Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe Asp Trp
100     100                 105                 110
102 aac aca ccc aag aaa ggt ggc agg agg tca cag tgg gtc cga aac tgg  620
103 Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg Asn Trp
104 115                 120                 125                 130
106 gct gtg tgg cgc tac ttt cga gac tac ttt ccc atc cag ctg gtg aag  668
107 Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys
108                 135                 140                 145
110 aca cac aac ctg ctg acc acc agg aac tat atc ttt gga tac cac ccc  716
111 Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro
112             150                 155                 160
114 cat ggt atc atg ggc ctg ggt gcc ttc tgc aac ttc agc aca gag gcc  764
115 His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala
116             165                 170                 175
118 aca gaa gtg agc aag aag ttc cca ggc ata cgg cct tac ctg gct aca  812
119 Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr
120             180                 185                 190
122 ctg gca ggc aac ttc cga atg cct gtg ttg agg gag tac ctg atg tct  860
123 Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
124 195                 200                 205                 210
126 gga ggt atc tgc cct gtc agc cgg gac acc ata gac tat ttg ctt tca  908
127 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu Ser
128             215                 220                 225
130 aag aat ggg agt ggc aat gct atc atc atc gtg gtc ggg ggt gcg gct  956
131 Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly Ala Ala
132             230                 235                 240
134 gag tct ctg agc tcc atg cct ggc aag aat gca gtc acc ctg cgg aac  1004
```

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135 Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu Arg Asn
136     245             250                 255
138 cgc aag ggc ttt gtg aaa ctg gcc ctg cgt cat gga gct gac ctg gtt  1052
139 Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp Leu Val
140     260             265                 270
142 ccc atc tac tcc ttt gga gag aat gaa gtg tac aag cag gtg atc ttc  1100
143 Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val Ile Phe
144 275             280                 285                 290
146 gag gag ggc tcc tgg ggc cga tgg gtc cag aag aag ttc cag aaa tac  1148
147 Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln Lys Tyr
148             295                 300                 305
150 att ggt ttc gcc cca tgc atc ttc cat ggt cga ggc ctc ttc tcc tcc  1196
151 Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser Ser
152             310                 315                 320
154 gac acc tgg ggg ctg gtg ccc tac tcc aag ccc atc acc act gtt gtg  1244
155 Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val Val
156             325                 330                 335.
158 gga gag ccc atc acc atc ccc aag ctg gag cac cca acc cag caa gac  1292
159 Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln Gln Asp
160     340             345                 350
162 atc gac ctg tac cac acc atg tac atg gag gcc ctg gtg aag ctc ttc  1340
163 Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys Leu Phe
164 355             360                 365                 370
166 gac aag cac aag acc aag ttc ggc ctc ccg gag act gag gtc ctg gag  1388
167 Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu
168             375                 380                 385
170 gtg aac tga gccagccttc ggggccaact ccctggagga accagctgca aatcactttt 1447
171 Val Asn
173 ttgctctgta aatttggaag tgtcatgggt gtctgtgggt tatttaaaag aaattataac 1507
175 aattttgcta aaccattaca atgttaggtc ttttttaaga aggaaaaagt cagtatttca 1567
177 agttctttca cttccagctt gccctgttct aggtggtggc taaatctggg cctaatctgg 1627
179 gtggctcagc taacctctct tcttcccttc ctgaagtgac aaaggaaact cagtcttctt 1687
181 ggggaagaag gattgccatt agtgacttgg accagttaga tgattcactt tttgccccta 1747
183 gggatgagag gcgaaagcca cttctcatac aagccccttt attgccacta ccccacgctc 1807
185 gtctagtcct gaaactgcag gaccagtttc tctgccaagg ggaggagttg gagagcacag 1867
187 ttgccccgtt gtgtgagggc agtagtaggc atctggaatg ctccagtttg atctcccttc 1927
189 tgccacccct acctcacccc tagtcactca tatcggagcc tggactggcc tccaggatga 1987
191 ggatggggggt ggcaatgaca ccctgcaggg gaaaggactg cccccatgc accattgcag 2047
193 ggaggatgcc gccaccatga gctaggtgga gtaactggtt tttcttgggt ggctgatgac 2107
195 atggatgcag cacagactca gccttggcct ggagcacatg cttactggtg gcctcagttt 2167
197 accttcccca gatcctagat tctggatgtg aggaagagat ccctcttcag aaggggcctg 2227
199 gccttctgag cagcagatta gttccaaagc aggtggcccc cgaacccaag cctcactttt 2287
201 ctgtgccttc ctgagggggt tgggccgggg aggaaaccca accctctcct gtgtgttctg 2347
203 ttatctcttg atgagatcat tgcaccatgt cagacttttg tatatgcctt gaaaataaat 2407
205 gaaagtgaga atccaaaaaa aaaaaaaaaa aa 2439
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 22
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
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213 <220> FEATURE:
215 <223> OTHER INFORMATION: PCR Primer
217 <400> SEQUENCE: 5
218 catacggcct tacctggcta ca                                    22
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 24
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 6
231 cagacatcag gtactccctc aaca                                  24
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 22
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
241 <223> OTHER INFORMATION: PCR Probe
243 <400> SEQUENCE: 7
244 tggcaggcaa cttccgaatg cc                                    22
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 19
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
254 <223> OTHER INFORMATION: PCR Primer
256 <400> SEQUENCE: 8
257 gaaggtgaag gtcggagtc                                        19
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
267 <223> OTHER INFORMATION: PCR Primer
269 <400> SEQUENCE: 9
270 gaagatggtg atgggatttc                                       20
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 20
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
280 <223> OTHER INFORMATION: PCR Probe
282 <400> SEQUENCE: 10
283 caagcttccc gttctcagcc                                       20
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 2262
288 <212> TYPE: DNA
289 <213> ORGANISM: M. musculus
291 <220> FEATURE:
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293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (207)...(1373)
297 <400> SEQUENCE: 11
298 ggtggccgcg cttcgctggc tttctgctca tctagggtgg cagcggctac ctacctcagc      60
300 tctcgccctg ctgccgccac ggcctgggcg ctgtccctca gctcccggag ctcagcgcga     120
302 agccctggcc ccggcggccg gggcatgggt caggggcgcg gcgtgaggcg gctttctgca     180
304 cggccgtgac gtgcattggc ttcagc atg aag acc ctc atc gcc gcc tac tcc     233
305                                Met Lys Thr Leu Ile Ala Ala Tyr Ser
306                                 1               5
308 ggg gtc ctg cgg ggt gag cgt cgg gcg gaa gct gcc cgc agc gaa aac     281
309 Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn
310  10              15              20              25
312 aag aat aaa gga tct gcc ctg tca cgc gag ggg tct ggg cga tgg ggc     329
313 Lys Asn Lys Gly Ser Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly
314              30              35              40
316 act ggc tcc agc atc ctc tca gcc ctc caa gac atc ttc tct gtc acc     377
317 Thr Gly Ser Ser Ile Leu Ser Ala Leu Gln Asp Ile Phe Ser Val Thr
318              45              50              55
320 tgg ctc aac aga tct aag gtg gaa aaa cag ctg cag gtc atc tca gta     425
321 Trp Leu Asn Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val
322         60              65              70
324 cta caa tgg gtc cta tcc ttc ctg gtg cta gga gtg gcc tgc agt gtc     473
325 Leu Gln Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Val
326     75              80              85
328 atc ctc atg tac acc ttc tgc aca gac tgc tgg ctg ata gct gtg ctc     521
329 Ile Leu Met Tyr Thr Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
330  90              95              100             105
332 tac ttc acc tgg ctg gca ttt gac tgg aac acg ccc aag aaa ggt ggc     569
333 Tyr Phe Thr Trp Leu Ala Phe Asp Trp Asn Thr Pro Lys Lys Gly Gly
334              110             115             120
336 agg aga tcg cag tgg gtg cga aac tgg gcc gtg tgg cgc tac ttc cga     617
337 Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr Phe Arg
338              125             130             135
340 gac tac ttt ccc atc cag ctg gtg aag aca cac aac ctg ctg acc acc     665
341 Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu Leu Thr Thr
342              140             145             150
344 agg aac tat atc ttt gga tac cac ccc cat ggc atc atg ggc ctg ggt     713
345 Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Met Gly Leu Gly
346      155             160             165
348 gcc ttc tgt aac ttc agc aca gag gct act gaa gtc agc aag aag ttt     761
349 Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu Val Ser Lys Lys Phe
350 170             175             180             185
352 cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg     809
353 Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met
354              190             195             200
356 cct gtg ctt cgc gag tac ctg atg tct gga ggc atc tgc cct gtc aac     857
357 Pro Val Leu Arg Glu Tyr Leu Met Ser Gly Gly Ile Cys Pro Val Asn
358              205             210             215
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VERIFICATION SUMMARY   DATE: 06/28/2005
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```
L:10   M:270 C: Current Application Number differs, Replaced Current Application No
L:10   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1241 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:3831 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:232
L:3846 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:233
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